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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:20:45 ; Search time 5.71318 Seconds

(without alignments)
798.574 Million cell updates/sec

Title: US-09-622-613B-24

Perfect score: 601
Sequence: 1 SNNATFOOKHIIITPICNT.....ICVKNQYVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	57.6	111	1	RNPO_RANCA
2	450	74.9	111	1	LECS_RANCA
3	369	61.4	111	1	RNPL_RANCA
4	272.5	45.3	104	1	RN30_RANPI
5	154.5	25.7	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	135.5	22.5	124	1	RNP_BALAC
8	135.5	22.5	145	1	ANGI_MOUSE
9	133.5	22.2	167	1	RNBR_BOVIN
10	132.5	22.0	124	1	RNP_PIG
11	128.5	21.4	151	1	RNBR_CARCA
12	127.5	21.2	123	1	ANG2_BOVIN
13	127.5	21.2	141	1	RNBR_GIRCA
14	127.5	21.2	151	1	RNBR_AXIPR
15	126.5	21.0	119	1	RNP_IGUIG
16	126.5	21.0	146	1	ANGI_CERAE
17	126.5	21.0	146	1	ANGI_MIOTA
18	125	20.8	146	1	ANGI_SATSC
19	123.5	20.5	143	1	RNBR_SHEEP
20	122.5	20.4	124	1	RNP_SHEEP
21	122	20.3	122	1	RNP_ANTRM
22	120.5	20.0	128	1	RNP_MACRU
23	120.5	20.0	147	1	ANGI_PONPY
24	120.5	20.0	149	1	RNP_MOUSE
25	120	20.0	146	1	ANGI_AOTTR
26	119.5	19.9	123	1	ANGI_PIG
27	118.5	19.7	128	1	RNBP_CAVPO
28	118	19.6	146	1	ANGI_SAGOE
29	117.5	19.6	128	1	RNP_HORSE
30	116.5	19.4	124	1	RNPICANDR
31	116.5	19.4	128	1	RNP_PROGU
32	115.5	19.2	146	1	ANGI_MACMU
33	114	19.0	148	1	ANGI_BOVIN

34	113.5	18.9	124	1	RNP_RANTA	P00666	rangifer ta
35	113.5	18.9	125	1	ANGI_RABIT	P11347	oryctolagus
36	113.5	18.9	146	1	ANGI_PAPHA	OBW654	papio hamad
37	113	18.8	147	1	ANGI_HUMAN	P03950	homo sapien
38	113	18.8	147	1	ANGI_PANTR	OBW658	pan troglod
39	112.5	18.7	124	1	RNP_CARCA	P00664	capreolus c
40	112.5	18.7	124	1	RNP_GIRCA	P00662	giraffa cam
41	112.5	18.7	148	1	RNL4_MOUSE	O9jjh1	mus muscicu
42	111.5	18.6	130	1	RNP_CRILLO	P24717	cricetus
43	111.5	18.6	147	1	RNL4_RAT	O55004	rattus norv
44	111.5	18.6	149	1	RNP_ACOCA	O9Wt55	acomys calh
45	110.5	18.4	124	1	RNP_AEPME	P07847	aepyceos m

ALIGNMENTS

RESULT 1	RNPO_RANCA	STANDARD:	PRT:	111 AA.
ID	RNPO_RANCA			
AC	P11916:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
DE	Rana catesbeiana (Bull. frog).			
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
RX	MEDLINE=67299649; PubMed=3304421;			
RA	Titani K., Takio K., Kawada M., Nitta K., Sakakibara F., Kawachi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) oocytes.";			
RL	Biochemistry 26:2189-2194(1987).			
RN	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes.";			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Sekiguchi K., Kawachi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs.";			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T. H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog).";			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE			
CC	AS SUBSTRATES, AND PREPERS THE FORMER. THE S-LECTIONS IN THE PROG			
CC	EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING			
CC	NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND			
CC	HUMAN ORIGIN.			
CC	-1- SUBUNIT: MONOMER.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
CC	PIR: A27121; A27121.			

DR PDB: 1BC4: 28-OCT-98.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Stalic acid; Lectin; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 SO SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 97.6%; Score 586.5; DB 1; Length 111;
 Best Local Similarity 99.1%; Pred. No. 1.2e-56;
 Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 NMATFOOKHIINPPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGYINMNV 60
 DB 2 NMAFPOKHITNTPTINCNTIMDNNIYVGGCKRVNFTFISSATYKAICTGYINMNV 61

QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 110
 DB 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

RESULT 2
 LEC3-RANCA
 ID LEC3-RANCA STANDARD; PRT: 111 AA.
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Stalic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=Egg;
 RX MEDLINE=9103319; PubMed=2229005;
 RA Kaniya Y., Oyama F., Oyama R., Sakakibara F., Nitte K., Kawachi H.,
 RT Takayanaagi Y., Tittani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs."
 RL J. Biochem. 108:139-143(1990).
 CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
 CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
 CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
 CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC PIR: JX0120; JX0120.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease; Stalic acid; Lectin.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97

FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 74.9%; Score 450; DB 1; Length 111;
 Best Local Similarity 78.2%; Pred. No. 6.7e-42;
 Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

QY 2 NMATFOOKHIINPPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGY-INMNV 59
 DB 2 NMAFPOKHITNTPTINCNTIMDNNIYVGGCKRVNFTFISSATYKAICTGASTNRNV 61

QY 60 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 109
 DB 62 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

RESULT 3
 RNPL-RANCA
 ID RNPL-RANCA STANDARD; PRT: 111 AA.
 AC P14626;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RT Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver."
 RL J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC PIR: JX0085; JX0085.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea. 1.
 DR ProDom: PD000535; RNaseA: 1.
 DR SMART: SM00092; RNase_Pc: 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; 1.
 DR HydroLase: Nuclease; Endonuclease.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 104 104
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.4%; Score 369; DB 1; Length 111;
 Best Local Similarity 65.5%; Pred. No. 3.8e-33;
 Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NMATFOOKHIINPPI-CNTIMDNNIYVGGCKRVNFTFISSATYKAICTGY-INMNV 59
 DB 2 NMAFPOKHITNTPTINCNTIMDNNIYVGGCKRVNFTFISSATYKAICTGASVSPRKE 61

QY 60 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 109
 DB 62 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVGCENQYVPHFAGIGRCP 111

ID	PN30_RANPI	STANDARD	PRT	104 AA.
AC	P22069.			
DT	01-AUG-1991 (Feb. 19, Created)			
DT	01-FEB-1994 (Feb. 28, Last sequence update)			
DT	01-FEB-1995 (Feb. 31, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (oncnase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91093131; PubMed=1985896;			
RA	Ardelet W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens			
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991)			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; PubMed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.,			
RA	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein:			
RT	a novel antitumor protein of Rana pipiens oocytes and early			
RT	embryos.";			
RL	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079; PubMed=8120892;			
RA	Mosimann S.C., Ardelet W., James M.N.G.;			
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an			
RT	amphibian ribonuclease with anti-tumor activity.";			
RL	J Mol. Biol. 236:1141-1153(1994)			
CC	-I- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY			
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR			
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH			
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-I- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC; 31-JAN-94.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA: 1.			
DR	Prodom: PD000535; RNaseA: 1.			
DR	SMART: SM00092; RNase_Pc: 1.			
DR	PROSITE: PS00127; RNase_PANCREATIC: 1.			
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.			
FT	MOD_RES	1		
FT	ACT_SITE	10	10	
FT	ACT_SITE	31	31	
FT	ACT_SITE	97	97	
FT	DISULFID	19	68	
FT	DISULFID	30	75	
FT	DISULFID	48	90	
FT	DISULFID	87	104	
FT	HELIX	3	10	
FT	HELIX	11	12	
FT	HELIX	19	22	
FT	TURN	23	24	
FT	TURN	26	30	
FT	TURN	33	38	
FT	TURN	41	48	
FT	HELIX	49	50	
FT	HELIX	55	58	
FT	STRAND	63	70	
FT	TURN	74	75	
FT	STRAND	77	84	
FT	STRAND	86	91	
FT	TURN	92	93	
FT	STRAND	94	101	
SEQUENCE	104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;			

Query Match	Similarity	45.3%	Score 272.5	DB 1	Length 104
Best Matches	54	Conservative	15	Mismatches	32
				Indels	9
				Gaps	4
Qy	2	NMATPFOOKHINT.PIICNTIMDNNTYVGGCKRVNTFIISATYKATCTGYT-MNMY	59		
Db	2	DWLFEQKKHINTFDDVDODNISTNLF- - -HCKDKNTFIYSRPEPKALICKGILASKNV	57		
Qy	60	LSTRFQULTCTRTSITPRCPPIYSKRETNICKCENQYVHFAGIGRC	109		
Db	58	LTTSEFYLSDC- - -NVTSRPCKRYKLKSTKNECVTCENQAPVHFVGWSC	104		
RESULT 5					
ANG3_MOUSE	STANDARD:	PRT:	145 AA.		
ID	ANG3_MOUSE				
AC	P97802:				
DI	01-NOV-1997 (Rel. 35, Created)				
DI	01-NOV-1997 (Rel. 35, Last sequence update)				
DI	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2) (Ef-5).				
GN	ANG3 OR ANGL.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RN	(1)				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BALB/c;				
RX	MEDLINE=97184476; PubMed=9032278;				
RA	Fu X., Kamps M.P.;				
RT	"E2a-Pbx1 induces aberrant expression of tissue-specific and developmentally regulated genes when expressed in NIH 3T3 fibroblasts."				
RL	Mol. Cell. Biol. 17:1503-1512(1997).				
CC	-1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (BY SIMILARITY)				
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
CC	-----				
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CC	-----				
DR	EMBL: U72672; AAC05794.1;				
DR	HSSP: P10152; 1AG1.				
DR	MGP: MGI:1201793; Angl.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; RNaseA; 1.				
DR	PRINTS: PR00794; RIBONUCLEASE.				
DR	ProDom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase; PC: 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; Angiogenesis;				
KW	Protein synthesis inhibitor; Signal.				
FT	SIGNAL	1	24	POTENTIAL.	
FT	CHAIN	25	145	ANGIOGENIN-3.	
FT	MOD_RES	25	25	PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).	
FT	ACT_SITE	37	37	BY SIMILARITY.	
FT	ACT_SITE	64	64	BY SIMILARITY.	
FT	ACT_SITE	137	137	BY SIMILARITY.	
FT	DISULFID	50	104	BY SIMILARITY.	
FT	DISULFID	63	115	BY SIMILARITY.	
FT	DISULFID	81	130	BY SIMILARITY.	
SO	SEQUENCE	145 AA;	16696 MW;	DE93BC9ZFLD682C CRC64;	

RESULT	9	
ID	RNBR_BOVIN	STANDARD: PRT: 167 AA.
AC	P39873;	
DT	01-FEB-1995 (Rel. 31, Created)	
DT	01-FEB-1995 (Rel. 31, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Ribonuclease, brain precursor (EC 3.1.27.-) (BRB) ..	
GN	BRN.	
OS	Bos taurus (Bovine).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC	Bovidae; Bovinae; Bos.	
OX	NCBI_TaxID=9913;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=92093604; Pubmed=1754384;	
RX	Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,	
RA	Viola M., Palmieri M., Russo E., Furla A.;	
RT	"Molecular cloning of the gene encoding the bovine brain ribonuclease	
RT	and its expression in different regions of the brain."	
RL	Nucleic Acids Res. 19:6469-6474(1991).	
RN	[2]	
RP	SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.	
RC	TISSUE=Brain;	
RX	MEDLINE=89214015; Pubmed=3243767;	
RA	Watanabe H., Katoh H., Ishii M., Komoda Y., Sando A., Takizawa Y.,	
RT	Ohgi K., Irie M.;	
RT	"Primary structure of a ribonuclease from bovine brain."	
RL	J. Biochem. 104:939-945(1988).	
RN	[3]	
RP	SEQUENCE OF 27-167 FROM N.A.	
RX	MEDLINE=96139017; Pubmed=8587129;	
RA	Confalone E., Bentuma J.J., Sasso M.P., Carsana A., Palmieri M.,	
RA	Vento M.T., Furla A.;	
RT	"Molecular evolution of genes encoding ribonucleases in ruminant	
RT	species."	
RL	J. Mol. Evol. 41:850-858(1995).	
CC	- 1. SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.	
CC	-----	
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CC	or send an email to license@sib-sib.ch).	
CC	-----	
DR	EMBL; X59767; CAA42439.1; -	
DR	EMBL; S81744; AAB36138.1; -	
DR	PIR; S20066; S20066.	
DR	PIR; JX0056; JX0056.	
DR	HSSP; P00656; 2RMS.	
DR	GlycoSuiteDB: P39873; -	
DR	InterPro; IPR001427; RNaseA.	
DR	Pfam; PF00074; RNaseA; 1.	
DR	PRINTS; PR00794; RIBONUCLEASE.	
DR	Prodom; PD000535; RNaseA; 1.	
DR	SMART; SM00092; RNase_Pc; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
KW	Hydroxylase; Nuclease; Endonuclease; Glycoprotein; Signal.	
FT	SIGNAL	1 26
FT	CHAIN	27 167
FT	ACT_SITE	38 38 RIBONUCLEASE, BRAIN.
FT	ACT_SITE	67 67 BY SIMILARITY.
FT	ACT_SITE	145 145 BY SIMILARITY.
FT	DISULFID	52 110 BY SIMILARITY.
FT	DISULFID	66 121 BY SIMILARITY.
FT	DISULFID	84 136 BY SIMILARITY.
FT	DISULFID	91 98 BY SIMILARITY.

FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 155 155 /FTID=CAR_0000005.
 FT CARBOHYD 159 159 O-LINKED.
 FT CONFLICT 155 155 T -> S (IN REF. 2).
 SQ SEQUENCE 167 AA: 18450 MW: 6181ACAC3CC2FC459 CRC64;

Query Match
 Best Local Similarity 31.4%; Pred. No. 1.5e-07;
 Matches 38: Conservative 17; Mismatches 43; Indels 23; Gaps 7;

OY 4 ATPQKH-----INPILCNTIMDNIIYIVGGQCKRVNFISSATTVAICGVINM 57
 Db 32 AKFRQHDSSSSSSNNYCNQMKRR-RMTHGRCKPVNTFVHESLDDVAVCS---QK 87
 OY 58 NVL-----STTRQLTCTRTSTTPRP-CPYSSRTETNYICVCKE-NOY-PVHEA 104
 Db 88 NITCKNGHPNCOYQSKSTWSTIDCRETGSSKYPNCAYKTSOKXITVACEGNPYPVHED 147
 OY 105 G 105
 Db 148 G 148

RESULT 10

RNP_PIG STANDARD: PRT: 124 AA.
 ID RNP_PIG
 AC P00671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RN51.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70104197; PubMed=5460946;
 RA Jackson R.L., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. II. The
 RT amino acid sequence of the reduced S-aminoethylated protein.";
 RL J. Biol. Chem. 245:637-653(1970).
 RN [2]
 RP REVISION TO 2.
 RA Wierenga R.K., Huizinga J.D., Gaastra W., Wellings G.W., Beintema J.J.;
 RT "Affinity chromatography of porcine pancreatic ribonuclease and
 RT reinvestigation of the N-terminal amino acid sequence.";
 RL FEBS Lett. 31:181-185(1973).
 RN [3]
 RP DISULFIDE BONDS.
 RX MEDLINE=70104198; PubMed=4904878;
 RA Phelan J.J., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. 3. The
 RT disulfide bonds.";
 RL J. Biol. Chem. 245:654-661(1970).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: A00816; NREG.
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW CARBOHYD Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84

FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 21 21
 FT CARBOHYD 34 34
 FT CARBOHYD 76 76
 SQ SEQUENCE 124 AA: 13804 MW: 0AC28CDE1411845 CRC64;

Query Match
 Best Local Similarity 31.6%; Pred. No. 1.4e-07;
 Matches 36: Conservative 19; Mismatches 42; Indels 17; Gaps 6;

OY 6 FOQKH-----INPILCNTIMDNIIYIVGGQCKRVNFISSATTVAICGVINM 57
 Db 8 FORQHDSSSSSSNNYCNLMMSRR-NMTHGRCKPVNTFVHESLDDVAVCSQINVCCK 66
 OY 59 VLSTTRQLT-----CTRTSTTPRP-CPYSSRTETNYICVCKENO--YPVHF 103
 Db 67 NGOTNCYQSNSTHMTIDCRGTGSSKYPNCAYKASQEQKHITVACEGNPYPVH 120

RESULT 11

RNBR_CAPCA STANDARD: PRT: 151 AA.
 ID RNBR_CAPCA
 AC P79351;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
 OS Capreolus capreolus (Roe deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Odocoileinae; Capreolus.
 OX NCBI_TaxID=9858;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278842; PubMed=9611269;
 RA Breukelman H.J., Van der Munnik N., Kleineldam R.G., Furia A.,
 RA Beintema J.J.;
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
 RL Gene 212:259-268(1998).
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: Y11673; CAA72371.1; -
 DR HSSP: P00656; ISRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR PRODOM: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
 FT ACT_SITE 41 41
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT CARBOHYD 62 62
 FT CARBOHYD 129 129
 FT CARBOHYD 133 133
 SQ SEQUENCE 151 AA: 16971 MW: 392D0E6302F006A6 CRC64;

Query Match 21.4% Score 128.5; DB 1; Length 151;
 Best Local Similarity 29.4%; Pred. No. 4.8e-07;
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;

OY 4 ATPOCKHIT-INTPTICNTIMDNNIYVGGCKRVNFTIISATYKAITCTGYNM 57
 DB 6 AKFRHMDSSSSSSGNNPCNOMMKRR-RMTHGRCKPVNPFVHESLDNVAVCS---QK 61
 OY 58 NVL-----STTRQLNCTRTSTTPP-CPYSSRTENYICVCKENQ--YVPHF 103
 DB 62 NITCKNGOPNCYQSNSTNMTIDCKRTGSSSKTPNCATKTSOKOKITYVACEDDPYVPHF 120

RESULT 12

ANG2_BOVIN STANDARD: PRT: 123 AA.

AC P80929; 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.27.-).

OS Bos taurus (Bovine);
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;

RP TISSUE=Serum, and Milk;
 RX MEDLINE=97409980; PubMed=9266695;
 RA Striydom D.J., Bond M.D., Vallée B.L.;

RT "An angiogenic protein from bovine serum and milk -- purification and
 RL Eur. J. Biochem. 247:535-544(1997)."

CC -I- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.

CC -I- TISSUE SPECIFICITY: SERUM, AND MILK.

CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR HSSP; P10152; IAGI.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase_Pc; 1.

DR PROSITE: PS00127; RNASE_PANCREATIC; 1.

KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Glycoprotein.

FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT ACT_SITE 12 12 BY SIMILARITY.

FT ACT_SITE 39 39 BY SIMILARITY.

FT ACT_SITE 113 113 BY SIMILARITY.

FT DISULFID 25 80 BY SIMILARITY.

FT DISULFID 38 91 BY SIMILARITY.

FT DISULFID 56 106 BY SIMILARITY.

FT CARBOHYD 33 33 N-LINKED (GLCNAC...).

SO SEQUENCE 123 AA; 14522 MW; B703B983919FD2P CRC64;

Query Match 21.2% Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 5e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

OY 6 FOQKHITP-ICNTIMDNNIYVGGCKRVNFTIISATYKAITCTGYNM 57
 DB 8 FLNRHYPSEFGHIDRCNTFMERR--NMTRPCKDTNFIHNSDDIAYVDDRNGEPR 65

OY 58 NVLSTTR--FOLNCTRTSTTPP-CPYSSRTENYICVCKENQYVPH 102
 DB 66 NGLRHSRSPFOVTCRHARGSPRPCRYRAFRANRVIVRCRDGPPI 113

RESULT 13

RNRB_GIRCA STANDARD: PRT: 141 AA.

AC Q29542; 029533; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).

OS Giraffa camelopardalis (Giraffe).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
 OC Giraffidae; Giraffa.
 NCBI_TaxID=9894;

RP SEQUENCE FROM N.A.

RX MEDLINE=96139017; PubMed=8587129;

RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmeri M.,
 RA Vento M.T., Furia A.;

RT "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species."

RL J. Mol. Evol. 41:850-858(1995).

CC SEQUENCE OF 31-114 FROM N.A.

RX MEDLINE=93367815; PubMed=8360916;

RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
 RA Carsana A., Palmeri M., Furia A.;

RT "Sequences related to the ox pancreatic ribonuclease coding region in
 RT the genomic DNA of mammalian species."

RL J. Mol. Evol. 37:29-35(1993).

CC -I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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DR EMBL; S81743; AAB36137.1; -

DR EMBL; S65126; AAB27931.1; -

DR HSSP; P00656; ZRNS.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA; 1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR PRODOM: PD000535; RNaseA; 1.

DR SMART: SM00092; RNase_Pc; 1.

DR PROSITE: PS00127; RNASE_PANCREATIC; 1.

KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.

FT ACT_SITE 41 41 BY SIMILARITY.

FT DISULFID 26 84 BY SIMILARITY.

FT DISULFID 40 95 BY SIMILARITY.

FT DISULFID 58 110 BY SIMILARITY.

FT DISULFID 65 72 BY SIMILARITY.

FT CARBOHYD 62 62 N-LINKED (GLCNAC...).

FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).

SO SEQUENCE 141 AA; 15592 MW; 73745FE9079591F CRC64;

Query Match 21.2% Score 127.5; DB 1; Length 141;
 Best Local Similarity 30.6%; Pred. No. 5.7e-07;
 Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY 4 ATPOCKHIT-INTPTICNTIMDNNIYVGGCKRVNFTIISATYKAITCTGYNM 57
 DB 6 AKFRHMDSSSSSSGNNPCNOMMKRR-RMTHGRCKPVNPFVHESLDNVAVCS---QK 61

OY 58 NVL-----STTRQLNCTRTSTTPP-CPYSSRTENYICVCKENQ--YVPHF 104
 DB 62 NITCKNGOPNCYQSNSTNMTIDCKRTGSSSKTPNCATKTSOKOKITYVACEDDPYVPHF 121

```

DB      122 G 122

RESULT 14
RNRB_AXIPR      STANDARD:      PRT:      151 AA.
ID      RNRB_AXIPR
AC      P87350:
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN      Brn.
OS      Axis porcinus (Hog deer).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC      Cervidae; Cervinae; Axis.
OX      NCBI_TaxID=57737;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98278842; PubMed=9611269;
RA      Breukelman H.J., van der Munnik N., Kleineldam R.G., Furia A.,
RA      Beintema J.J.;
RT      "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL      Gene 212:259-268(1998).
CC      -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: Y11670; CAI72368.1; -.
DR      HSSP: P00656; 1SRN.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA.1.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA.1.
DR      SMART: SM00092; RNase_Pc.1.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT      ACT_SITE 41
FT      DISULFID 26
FT      DISULFID 40
FT      DISULFID 58
FT      DISULFID 65
FT      CARBOHYD 62
FT      CARBOHYD 129
FT      CARBOHYD 133
SQ      SEQUENCE 151 AA; 16819 MW; E95F3757FEC5B233 CRC64;

Query Match      21.2%; Score 127.5; DB 1; Length 151;
Best Local Similarity 30.8%; Pred. No. 6.2e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

OY      4 ATFOOKHI-----INPIICNTIMDNIIYVGGCKRVNFTIISATTVAICGVLM 57
DB      6 AKFRROMHDAGSSSSGNSNYCNQMKRR-RMTHGRCQVNTFVHESLDSVAKVCS--QK 61
OY      58 NVL-----STTRFOLNTCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHFA 104
DB      62 NITCKNCPNCGNSSTWNTITDCRETGSSKYPNCAYKTSQKQKITVACGDNPVYVPHFD 121
OY      105 G 105
DB      122 G 122

RESULT 15
RNP_IGUG

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ID      RNP_IGUG      STANDARD:      PRT:      119 AA.
AC      P80287;
DT      01-FEB-1994 (Rel. 28, Created)
DT      01-FEB-1994 (Rel. 28, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS      Iguana iguana (Common Iguana).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX      NCBI_TaxID=8517;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Pancreas;
RX      MEDLINE=8307028;
RA      Zhao W., Beintema J.J., Hofsteenge J.;
RT      "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT      ribonuclease.";
RL      Eur. J. Biochem. 219:641-646(1994).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: PANCREAS.
CC      -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR      HSSP: P00656; 1LSO.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA.1.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA.1.
DR      SMART: SM00092; RNase_Pc.1.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolyase; Nuclease; Endonuclease.
FT      MOD_RES 1
FT      DISULFID 25
FT      DISULFID 39
FT      DISULFID 57
FT      ACT_SITE 10
FT      ACT_SITE 40
FT      ACT_SITE 113
SQ      SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match      21.0%; Score 126.5; DB 1; Length 119;
Best Local Similarity 29.8%; Pred. No. 6.2e-07;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

OY      2 NMATFOOKHI-----INPIICNTIMDNIIYVGGCKRVNFTIISATTVAIC--- 51
DB      2 DWSSFOKNHDIYPTTSASNPAYCDLMMQRR-NLNPTRCKTRNFTVHASPSEIDQVCGSG 60
OY      52 -TGVINMNVLSSTTRFOLNTCTRTSIT-PRCPYSSRTETNYICVKEHQYVPHF 103
DB      61 GTHEDNLVDNENSPDLIDCKNVGTVAPSSCKYNGTPTKRIIRIACENQPVPHF 114

Search completed: June 25, 2003, 14:50:07
Job time : 5.71318 secs

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